

Conor R. Walker

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Education

University of Cambridge, UK

2017–2021

PhD in Computational Biology

- Thesis: Statistical analysis of short template switch mutations in human genomes
- Advisers: Nick Goldman, Aylwyn Scally, Nicola De Maio

Newcastle University, UK

2016–2017

MSc Bioinformatics · first-class honours (83%)

- Thesis: Optimising nucleic acid sequences for DNA strand displacement systems
- Adviser: Harold Fellermann

Liverpool John Moores University, UK

2013–2016

BSc (Hons) Zoology · first-class honours (80%)

- Thesis: The genetics of insecticide resistance in the blackfly *Simulium vittatum*
- Advisers: Craig Wilding, Will Swaney

Research experience

New York Genome Center, USA

Jan. 2022–Present

Postdoctoral Research Associate · G² Lab

- I work on privacy-preserving methods for analysing single-cell RNA sequencing data

European Bioinformatics Institute (EMBL-EBI), UK

2017–2022

Predocctoral Researcher

- I developed statistical methods to identify template switch variants in DNA sequences
- I characterised the human evolutionary, population, and cancer landscape of template switch mutagenesis
- I designed convolutional neural networks for accurately detecting between-species positive selection, validated through large-scale simulation of training and testing data

This work was funded by both EMBL and NIHR BRC.

Newcastle University, UK

2016–2017

Postgraduate Student Research

- I implemented multi-objective genetic algorithms for designing and optimising DNA sequences for use in DNA computing systems

Liverpool John Moores University, UK

2016

Undergraduate Student Research

- I identified enzyme families and point mutations associated with insecticide resistance in a medically-important blackfly genome using phylogenetic methods

Publications

Peer-reviewed

Mutation rates and selection on synonymous mutations in SARS-CoV-2.

De Maio N., [Walker C. R.](#), Turakhia Y., Lanfear R., Corbett-Detig R., Goldman N.

[Genome Biology and Evolution](#) 13, [evab087](#) (2021).

Short-range template switching in great ape genomes explored using pair hidden Markov models.

[Walker C. R.](#), Scally A., De Maio N., Goldman N.

[PLOS Genetics](#) 17, [e1009221](#) (2021).

Stability of SARS-CoV-2 phylogenies.

Turakhia Y., De Maio N., Thornlow B., Gozashti L., Lanfear R., [Walker C. R.](#), Hinrichs A. S., Fernandes J. D., Borges R., Slodkowitz G., Weilguny L., Haussler D., Goldman N., Corbett-Detig R.

[PLOS Genetics 16, e1009175](#) (2020).

A phylodynamic workflow to rapidly gain insights into the dispersal history and dynamics of SARS-CoV-2 lineages.

Dellicour S., Durkin K., Hong S. L., Vanmechelen B., Martí-Carreras J., Gill M. S., Meex C., Bontems S., André E., Gilbert M., [Walker C. R.](#), De Maio N., Faria N. R., Hadfield J., Hayette M., Bours V., Wawina-Bokalanga T., Artesi M., Baele G., Maes P.

[Molecular Biology and Evolution 38, 1608–1613](#) (2020).

Preprint/equivalent

phastSim: efficient simulation of sequence evolution for pandemic-scale datasets.

De Maio N., Boulton W., Weilguny L., [Walker C. R.](#), Turakhia Y., Corbett-Detig R., Goldman N.

[bioRxiv, doi.org/10.1101/2021.03.15.435416](#) (2021).

Masking strategies for SARS-CoV-2 alignments.

De Maio N., [Walker C. R.](#), Borges R., Weilguny L., Slodkowitz G., Goldman N.

[virological.org/t/masking-strategies-for-sars-cov-2-alignments/480](#) (2020).

Issues with SARS-CoV-2 sequencing data.

De Maio N., [Walker C. R.](#), Borges R., Weilguny L., Slodkowitz G., Goldman N.

[virological.org/t/issues-with-sars-cov-2-sequencing-data/473](#) (2020).

Selected presentations

ISMB/ECCB 2021

Jul. 2021

Talk: Accurate detection of positive selection using convolutional neural networks

[Walker C. R.](#), De Maio N., Goldman N.

SMBE 2021

Jul. 2021

Talk: Accurate detection of positive selection using convolutional neural networks

[Walker C. R.](#), De Maio N., Goldman N.

Evolution 2021

Jun. 2021

Talk: Accurate detection of positive selection using convolutional neural networks

[Walker C. R.](#), De Maio N., Goldman N.

SMBE 2019

Jul. 2019

Poster: Short template switches explain mutation clusters in the human genome

[Walker C. R.](#), De Maio N., Goldman N.

NIHR BRC Annual Research Day

Jul. 2018

Talk: Investigating short template switch mutations in humans and model organisms

[Walker C. R.](#)

Phylogroup XI

Mar. 2018

Talk: Short template switch events explain mutation clusters in the human genome

[Walker C. R.](#), Löytynoja A., Goldman N.

Teaching

Students supervised

Fatma Rabia Fidan

2021

- Masters-level project: Identifying *de novo* template switch mutations in trios of human genomes

Shayesteh Arasti (co-advised with Nicola De Maio)

2021

- Masters-level project: Using convolutional neural networks to detect positive selection

Viacheslav Vasilev (co-advised with Nicola De Maio)	2020
• Masters-level project: Using convolutional neural networks to detect positive selection	
William Xu (co-advised with Nicola De Maio)	2020
• Masters-level project: Using convolutional neural networks to detect positive selection	
Teaching assistant	
Medics to Coders · University of Cambridge, UK	2018
• I helped to deliver practical sessions on programming in Python at the School of Clinical Medicine	

Honours and awards

Best student talk	May 2019
• Audience vote at the annual EMBL-EBI PhD Seminar Day	
Outstanding performance by a MSc Bioinformatics programme student	Oct. 2017
• Awarded for achieving the highest overall grade on my master's degree programme	
Zoology prize	Sep. 2016
• Awarded for achieving the highest overall grade on my bachelor's degree programme	

Other scientific activities

Committees

Student Representative · EMBL-EBI, UK	2018–2020
• Attended meetings with senior management from across all EMBL outstations to discuss issues impacting the graduate community at EMBL	
• Organised a variety of academic and social events within the institution	
Graduate Student and Post-Doc Forum member · University of Cambridge, UK	2018
• I worked as part of a group of students and postdocs to devise strategies for creating a more positive experience for graduate students in the School of Life Sciences	

Memberships

International Society for Computational Biology
 Society for Molecular Biology and Evolution
 Society for the Study of Evolution

Reviewer for

Nature Medicine
 Molecular Biology and Evolution
 BMC Bioinformatics

Skills

Programming	Python, Bash, C++, R, AWK, LaTeX
Libraries	Numpy, SciPy, Keras, TensorFlow, PyTorch, scikit-allel, matplotlib, seaborn
Coding practices	Git, Snakemake, unit testing, Docker, Singularity, Jupyter, Vim
High performance computing	Daily use of both CPU and GPU clusters in a LSF environment
Operating systems	Linux, MacOS